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(POS-35) Modeling the cooperative compaction of bacterial chromosomes by biomolecular crowding and the cross-linking protein H-NS

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The way chromosomes are spatially organized influences their biological functions. Cells orchestrate the action of various molecules toward organizing their chromosomes: chromosome-associated proteins and the surrounding “free” molecules often referred to as crowders. Chain molecules like chromosomes can be entropically condensed in a crowded medium. A number of recent experiments showed that the presence of the protein H-NS enhances the entropic compaction of bacterial chromosomes by crowders. Using a coarse-grained computational model, we discuss the physical effects on bacterial chromosomes H-NS and crowders bring about. In this discussion, a H-NS dimer is modeled as a mobile binder with two binding sites, which can bind to a chromosome-like polymer with characteristic binding energy. Using the model, we will clarify the relative role of biomolecular crowding and H-NS in condensing a bacterial chromosome, offering quantitative insights into recent chromosome experiments. In particular, they shed light on the nature and degree of crowder and H-NS synergetics: while the presence of crowders enhances H-NS binding to a bacterial chromosome, the presence of H-NS makes crowding effects more efficient, suggesting two-way synergetics in condensing the chromosome.

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computational modeling

Keyword-2

chromosome organization

Keyword-3

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